From: <u>Jay Field</u>

To: <u>Burt Shephard/R10/USEPA/US@EPA</u>

Cc: <u>Eric Blischke/R10/USEPA/US@EPA; Robert Gensemer; Robert Neely</u>

Subject: Re: Summary of Sediment Bioassay Interpretation Resolution

Date: 07/14/2009 02:03 PM

Attachments: PH Tox Ref 090313 compare.xls

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thanks, that is what I am finding also. we carried more figures and rounded later. the differences are in both directions and are only for the biomass endpoints. attached is a spreadsheet comparing the results and showing the differences.
 Shephard.Burt@epamail.epa.gov wrote:
 > Jay,
 I might be able to save you a little bit of time. The raw data discrepancies appear to be due to either minor differences in rounding or significant digits, or in the case of the two stations with duplicate results, failure to use the arithmetic mean of the two data points as the single point for the station.
> I think what has happened on some of the rounding is due to a difference in how they calculated the growth and biomass responses relative to control response. Using the 2006 benthic interpretive report as an example, LWG historically calculated growth relative to control as (C - T) / C, where C and T are the control sample and test sample growth, respectively. Currently, LWG is calculating biomass (a different endpoint as per our previous direction) relative to control as T / C. The earlier formula (C - T) / C gives the proportional reduction in growth relative to control, not the proportion of control growth. To convert the proportional reduction in growth relative to control to the desired proportion of control growth (now biomass) requires an extra calculation step that seems to be adding some of the observed rounding errors and differences between us and LWG. A quick hypothetical example using C = 100 and T = 90 for the two equations will show you the difference in the results of the two formulas, and why the older formula requires an additional calculation step to yield the desired proportion of control growth value.
      of control growth value.
      One thing I didn't check is the accuracy of their summing of the individual growth values to see if the biomass values are correct, so you might start there.
 > Best regards,
 > Burt Shephard
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      "If your experiment needs statistics to analyze the results, then you
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Neely <Robert.Neely@noaa.gov
                                                                                                                                                                                                      Subject
                                                                                                                        Re: Summary of Sediment Bioassay
Interpretation Resolution
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> Eric et al, > I agree with Bob G's observations. I am in the process of comparing > values for the 4 bioassay endpoints and have identified a couple of > discrepancies---some appear to be rounding, others related to treatment > of the replicates from the R3 tests, and a couple of others that I need > to go back to original data. When I finish with this process (hopefully > later today), I will distribute the table of values for the 17 reference

> stations. > one issue with the replicate tox results for G786 and G788: one of the
> replicate results for 786 did not qualify as reference sample based on
> the criteria established, but the average of the results did qualify.
> In my treatment of the reference samples, I averaged the results for
 each of the control-normalized results for each endpoint for each of the
> two replicate pairs. I do not recall any specific guidance about
> treatment of replicates, but I recall raising the issue. I also support Bob's point about the best fit for 5th pctile, not necessarily the best overall fit. My recommendation is that EPA do the curve-fitting, determine the values, and provide a table of values to use for the thresholds. This would save all of us time and we could move on to more important issues (like what are we going to do with those values) those values). Jay Robert Gensemer wrote: Eric: A few observations from my perspective: 2) The control-normalization looks correct for biomass, but if I recall (I don't have my files with me at the moment) that LWG's biomass values for individual stations did not quite match values $\frac{1}{2}$ that Jay derived for table RE-1. 3) You have the control normalization correct (test/control) but 3) You have the control normalization correct (test/control) but we need to be careful to recommend use of survivorship, not mortality, to be fully consistent with our guidance and numeric examples. I realize Table 2-1 used mortality, but we have been very consistent all along that we need to use survivorship, and from a recent call with Burt, Don McD. agrees that control-normalized survivorship is the correct value to use, not ctrl-norm mortality. Yes, they relate directly (or should I say, inversely) to one another, but the 5th percentile calculation could be different using one vs. the other, so we need to be consistent, and use survivorship. could be different using one vs. the other, so we need to be consistent, and use survivorship.

4) I could not find any explicit guidance regarding the duplicate RE samples. Its not in the McDonald report that I can find, and I don't think we went into this level of detail in the problem formulation. It may be one of those things that just seemed very obvious to all of us, and so never felt the need to explicitely direct it. Actually, it may have only come up, to my recollection, during our own RE calculations in March. So table RE-1 definitely reflects this approach, although I don't think it was spelled out in the text. reflects this approach, although I don't think it was spelled out in the text.

6) I agree with your summary here, except to say that we need to not just chose the best overall curve fit, but particularly in the case of Hyalella biomass, we need a curve that fits the lower tail (i.e., 5th %ile) of the distribution best. For the other three endpoints, this is probably not an issue (i.e., best fit is also best 5th %ile fit). But for Hyl biomass, we need to think more carefully about what distribution fits at the lower tail of the distribution. I think this is a valid approach that makes the best out of the available data. LWG's curve fit created a 5th %ile value that was quite a bit lower than the empirical numbers; I do not think that was the most appropriate representation of the data. data. Parametrix 40th Anniversary, 1969-2009 inspired people . inspired solutions . making a difference Robert W. Gensemer, Ph.D.
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rgensemer@marganeric.com rgensemer@parametrix.com b Before printing, please think green. From: Blischke.Eric@epamail.epa.gov [Blischke.Eric@epamail.epa.gov Sent: Monday, July 13, 2009 5:02 PM
To: Robert Gensemer; Shephard.Burt@epamail.epa.gov;
jay.field@noaa.gov; Goulet.Joe@epamail.epa.gov
Cc: Humphrey.Chip@epamail.epa.gov
Subject: Summary of Sediment Bioassay Interpretation Resolution As you are aware, we have been discussing some of the details of the LWG's interpretation of the Portland Harbor sediment bioassay results. Some elements of the interpretation were discussed during a conference call on Thursday, June 18, 2009. Here is where I believe we are: 1) No transcription errors were identified during a review of the reference envelope bioassay results.
2) The total biomass calculations were done correctly.
3) Mortality should be computed as test/control. This is consistent with Table 2-1 in the March 17, 2006 Bioassay Interpretation Report, ASTM Method E-1706, and EPA Guidance.
4) Duplicate reference envelope samples should be pooled (averaged) rather than treated as individual samples. This is consistent with February 15, 2008 problem formulation (Note: is

this the correct reference? I could not find this in either the problem formulation nor the MacDonald benthic risk evaluation)
5) Identification of Level 1, Level 2 and Level 3 thresholds:
The toxicity thresholds should be calculated based on 10% of the reference envelope not an absolute 10%. This is consistent with Tables RE 1, RE-2 and the text of EPA's March 31, 2009 direction on the Calculation and Use of Reference Envelope for Portland Harbor Sediment Toxicity Test Interpretation
6) Identification of the 5% of the reference envelope should be accomplished using a range of curve fitting procedures appropriate for the data set distribution. The curve fitting procedure with the best overall fit should be selected and the 5% calculated using the best fit curve fitting procedure.

The above procedures for computing the results of the bioassay tests, calculating hit/no-hit designations, developing the reference envelope and identifying Level 1, Level 2 and Level 3 toxicity hits should be followed.

Please look this over and make sure it matches up with the reference duplicate samples. Once everyone agrees with the outlined procedures. See also my note about the pooling of the reference duplicate samples. Once everyone agrees with the outlined procedures, I will send an email to the LWG summarizing this and recommending a conference call to discuss if there area any questions.

Thanks, Eric

--Jay Field
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